———. 1978. A critical review of the models of group selection. Q. Rev. Biol. 53:101–114.
———. 1979. The primary characteristics of *Tribolium* populations group selected for increased and decreased population size. Evolution 33:749–764.
———. 1980. An experimental study of kin selection. Evolution 34:844–855.
———. 1982. Group selection: migration and the differentiation of small populations. Evolution 36:949–961.
———. 1985. The effects of genotypic interactions on evolution in structured populations. Pp. 280–293 *in* V. L. Choopra, ed. Genetics: new frontiers. Proceedings of the XV International Congress of Genetics. Oxford and IBH Publishing, New Delhi, India.
———. 1992. Sewall Wright: gene interaction in the shifting balance theory. Pp. 35–62 *in* J. Antonovics and D. Futuyma, eds. Oxford surveys of evolutionary biology. Vol. 6. Oxford Univ. Press, New York.
———. 2000. Epistasis: genetic constraint within. populations and accelerant of divergence among them. Ch. 12. *in* J. B. Wolf, E. D. Brodie III, and M. J. Wade, eds. Epistasis and the evolutionary process. Oxford Univ. Press, New York. *In press.*
Wade, M. J., and C. J. Goodnight. 1991. Wright's shifting balance theory: an experimental study. Science 253:1015–1018.
———. 1998. The theories of Fisher and Wright in the context of metapopulations: when nature does many small experiments. Evolution 52:1537–1553.
Wade, M. J., and J. R. Griesemer. 1998. Populational heritability: empirical studies of evolution in metapopulations. Am. Nat. 151: 135–147.
Wade, M. J., and S. Kalisz. 1990. The causes of natural selection. Evolution 44:1947–1955.
Wade, M. J., and D. E. McCauley. 1980. The phenotypic and genotypic differentiation of small populations. Evolution 34: 799–812.
———. 1984. Group selection: the interaction of local deme size and migration on the differentiation of small populations. Evolution 38:1047–1058.
Wade, M. J., Y. Toquenaga, and N. Johnson. 1999. Intraspecific genotype-environment variation affecting the expression of Haldane's Rule in hybrids between flour beetle species. Evolution 53:855–865.
Wagner, A., G. P. Wagner, and P. Similion. 1994. Epistasis can facilitate the evolution of reproductive isolation by peak shifts: a two-locus two-allele model. Genetics 138:533–545.
Warren, D. C. 1974. Breeding. Pp. 248–276 *in* O. A. Hanke, J. L. Skinner, J. H Florea, eds. American Poultry History 1823–1973. American Printing and Publishing, Madison, WI.
Williams, G. C. 1966. Adaptation and natural selection. Princeton Univ. Press, Princeton, NJ.
Wimsatt, W. 1980. Reductionistic resarch strategies and their biases in the units of selection controversy. Pp. 213–259 *in* T. Nickles, ed. Scientific discovery: case studies. Reidel, Dordrecht, The Netherlands.
Wolf, J. B. 2000. Indirect genetic effects and gene interactions. Ch. 10 *in* J. B. Wolf, E. D. Brodie III, and M. J. Wade, eds. Epistasis and the evolutionary process. Oxford Univ. Press, New York. *In press.*
Wolf, J. B., and E. D. Brodie III. 1998. Coadaptation of parental and offspring characters. Evolution 52:299–308.
Wolf, J. B., E. D. Brodie III, J. M. Cheverud, A. J. Moore, and M. J. Wade. 1998. Evolutionary consequences of indirect genetic effects. Trends Ecol. Evol. 13:64–69.
Wolf, J. B., E. D. Brodie III, and A. J. Moore. 1999. Interacting phenotypes and the evolutionary process II: selection resulting from social interactions. Am. Nat. 153:254–266.
Wolf, J. B., E. D. Brodie III, and M. J. Wade, eds. 2000. Epistasis and the evolutionary process. Oxford Univ. Press, New York. *In press.*
Wright, S. 1945. Tempo and mode in evolution: a critical review. Ecology 26:415–419.
———. 1959. Physiological genetics, ecology of populations, and natural selection. Persp. Biol. Med. 3:107–151.
———. 1969. Evolution and the genetics of populations. Vol. 2. Univ. of Chicago Press, Chicago, IL.

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VARYING MIGRATION AND DEME SIZE AND THE FEASIBILITY OF THE SHIFTING BALANCE

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Taking some comfort in the adage ''If you aren't making mistakes, then the problems you're working on are too easy,'' we admit to the technical errors identified by Coyne et al. (2000) and will like to use this opportunity primarily to remediate some weaknesses in our original paper (Peck et al. 1998). We commend Coyne et al. (2000) for taking a constructive approach and essentially telling us how to produce more convincing evidence for our assertions, which we are pleased to begin doing here. However, before getting to these specifics, we want to emphasize that we are not (and were not) arguing for shifting balance (SBT) as the dominant mode for the evolution of adaptations, but simply against what we still believe to be a premature general verdict of ''case closed.''

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First, we present some simulation results that further support our assertion that the progress of phase III can be facilitated by two factors that have been given scant attention in the theoretical literature on SBT: stochastic migration and random variation in deme size. Coyne et al. (2000) write ''Peck et al. provide no comparison between simulations with and without stochastic migration, so it is unclear what effect such migration would have,'' and that ''Peck et al. (1998) provide no support for their conjecture that stochastic migration has a significant effect on phase III.'' However, table 2 of Peck et al. (1998) shows phase III proceeding for several parameter combinations where the expected number of migrants per generation is much less than one. Recall that our model tracks discrete individuals at all times, so in a deterministic-migration analog of our model, there would be no migration whatsoever (i.e., our model does not admit migration of fractional individuals) and phase III could not proceed. In these cases, stochastic migration is clearly having a substantial effect.

Some limited simulations of our model on a small spatial grid indicate that the effect of stochastic migration persists at higher migration rates where several migrants per generation are expected. However, the time constraints on this manuscript do not allow us to map out the parameter range where this occurs or to repeat our simulations on a larger spatial grid as suggested by Coyne et al. (2000). We therefore consider here the two-deme model from our original paper. This model caricatures an incremental step in phase III, where deme 1 has become fixed for the more fit genotype (*AA*) and sends migrants into adjacent deme 2, where the less fit genotype (*aa*) is initially fixed. Because migration is one-way only, this reduces to a single-deme model in which the sequence of events is as follows: (1) parents in generation t (with allele A at frequency $p_A[t]$) mate randomly and produce offspring in Hardy-Weinberg proportions; (2) viability selection occurs on offspring, with fitnesses $(1 + k)$, $(1 - s)$, 1 for genotypes *AA*, *Aa*, *aa*, respectively; (3) some number $m(t)$ of selected offspring, chosen at random, are replaced by an equal number of immigrants having genotype *AA*, and these together comprise the parents in generation $t + 1$. Deme size N(t) is finite in the model and potentially varying over time, with median **N.** Steps 1 and 2 were implemented in the simulations by choosing the $N(t)$ genotypes for surviving offspring independently from a trinomial distribution in relative proportions $p_{AA}^2(1 + k):2p_A(1 - p_A)(1 - s):(1 - p_A)^2$. In *deterministic migration* simulations, $m(t)$ was constant at value **mN,** where **m** is the mean migration rate. In *stochastic migration* simulations, $m(t)$ was chosen at random each generation from the binomial distribution with parameters **N** and **m.** In the *varying deme size* simulations, $N(t)$ followed a log-normal distribution (rounded up to the nearest integer) with $\log N(t) = \log\mathbf{N} + \sigma z(t)$ and $z(t)$ being a first-order Gaussian autoregressive process with unit variance and autocorrelation ρ. As a result, the effective migration rate $\mathbf{mN}/N(t)$ also followed (apart from rounding) a log-normal distribution with $\log(\mathbf{mN}/N[t])$ having variance σ^2 and autocorrelation ρ. Varying deme size simulations also included stochastic migration.

Table 1 shows some results for median deme sizes $\mathbf{N} = 100$ and $\mathbf{N} = 200$, for a range of values of the selection coefficient s and the mean migration rate **m.** Values in the table are the median time to fixation of the *AA* genotype in the second deme, based on 101 replicate simulation runs of 20,000 generations. The selection coefficient k was chosen as a function of s so that fixation of *AA* occurs deterministically (i.e., in the mean-field model with constant migration and no drift) for $\mathbf{m} = 0.05$ or larger. The standard deviation of $\log N(t)$ was set at 0.5, which according to Connell and Sousa (1983) and Root and Cappucino (1992) is a typical value for the variability of local population size over time.

TABLE 1. Time to fixation of the *AA* allele in the second deme, for simulations with deterministic migration, stochastic migration, and stochastic migration with varying deme size. Values in the table are the median time to fixation in 101 simulation runs, terminated at 20,000 generations. An asterisk indicates that fixation had not occurred after 20,000 generations in more than half of the runs. Deme size variations were log-normally distributed, such that $\log N(t)$ was normally distributed with mean = log**N**, standard deviation $\sigma = 0.5$, and autocorrelation $\rho = 0.75$; s, selection coefficient; **m**, mean migration rate.

s	**m**	Deterministic migration	Stochastic migration	Varying deme size
N = 100				
0.5	0.05	68	50	34
	0.04	773	293	59
	0.03	*	7700	121
	0.02	*	*	853
	0.01	*	*	15354
0.7	0.05	51	35	25
	0.04	438	122	39
	0.03	*	2990	62
	0.02	*	*	287
	0.01	*	*	5585
0.9	0.05	34	25	18
	0.04	281	75	25
	0.03	*	818	52
	0.02	*	*	192
	0.01	*	*	2376
N = 200				
0.5	0.05	79	83	34
	0.04	11591	2873	61
	0.03	*	*	155
	0.02	*	*	1636
	0.01	*	*	*
0.7	0.05	53	40	24
	0.04	6561	449	33
	0.03	*	*	88
	0.02	*	*	700
	0.01	*	*	*
0.9	0.05	42	30	17
	0.04	3947	305	24
	0.03	*	*	66
	0.02	*	*	325
	0.01	*	*	8743

In these simulations, drift alone allowed the fitter genotype to spread for **m** slightly below 0.05. With stochastic migration, the range of mean migration rates allowing spread of the fitter genotype was slightly broadened, while the combination of stochastic migration with population fluctuations allowed the more fit genotype to spread (albeit less quickly) for migration rates as low as $\mathbf{m} = 0.01$. The large effect of varying deme size is due to the fact that from the perspective of the recipient deme, it also causes variation in the effective migration rate (number of immigrants relative to number in the deme). When the effective migration rate is (temporarily) high, the frequency of the fitter allele can increase past the

threshold, where it will continue to increase deterministically even when the effective migration rate drops.

In our model the expected number of immigrants is constant at **mN,** which amounts to tacitly assuming that the donor deme size is constant at **N.** If the donor and recipient deme sizes fluctuate in synchrony, then the effect of varying deme size vanishes. Conversely, if the two demes fluctuate out of synchrony, the effect of varying deme size would be larger than in the simulations reported in Table 1. Additional simulations (not reported here) with covarying deme sizes conform with this expected trend: As the between-deme correlation drops to zero, so does the expected time to fixation of the fitter allele in the recipient deme. Asynchronous fluctuation of deme sizes is not an unreasonable assumption. For example, in a six-year study of 23 phytophagous insect species associated with goldenrod in the Finger Lakes region of New York, Root and Cappucino (1992, p. 412) found that ''most of the time populations of a given species are fluctuating independently,'' and similar observations have been made for other insect species (Cappucino and Price 1995).

As Coyne et al. (2000) reiterate, the theoretical conflict between phases I and III is that migration must simultaneously be low enough for phase I and high enough for phase III. At least for the parameter values considered here, stochastic migration and population fluctuations allow phase III to proceed at much lower migration rates than otherwise. Reverse peak shifts (from fixation of *AA* to fixation of *aa*) still typically require higher levels of migration. As in our simulations, consider the two-deme model with selection coefficients s and k such that the more fit allele can spread deterministically from deme 1 to deme 2 if the mean migration rate is $\mathbf{m} = 0.05$ or higher. Then the migration rates required for a shift in the opposite direction (i.e., with the donor deme fixed for the less fit allele, and the recipient deme initially fixed for the more fit allele) are $\mathbf{m} = 0.13$ at $s = 0.5$, $\mathbf{m} = 0.25$ at $s = 0.7$, and $\mathbf{m} = 0.36$ at $s = 0.9$. Thus the necessary conditions for nonadaptive reverse peak-shifts are considerably more restrictive than those for adaptive peak shifts (and even more so if differential migration is admitted into the theory). Of course, it remains a conjecture that these properties will persist in a full spatial model, but the intuition is transparent enough that the conjecture seems reasonable.

Coyne et al. (2000) suggest that the proper comparison for our simulation model is with Barton and Rouhani (1991). We agree that in appropriate parameter ranges our simulations should replicate the scaling relations derived in that paper, if only as a check on our programming. However, Barton and Rouhani (1991) ''concentrate on the case where migration is high enough for the population to be effectively continuous'' (p. 500), meaning that allele frequencies on a discrete grid can be approximated by a smooth function of spatial location; their analytic results are for ''the limit of weak selection and large population size'' (p. 503). Our interest is more in the prototypical SBT situation where the favorable allele combination initially becomes fixed in a single deme and then spreads by a deme-by-deme series of fixations. As Barton and Rouhani (1991, p. 500) describe, this occurs under different assumptions (about the relative magnitudes of selection and migration) from those assumed in deriving their scaling relations. An additional complication is that, as Barton and Rouhani (1991) note, the fixation probability in their model is highly sensitive to the spatial topology and distance between demes. It is thus not clear to us that Barton and Rouhani's (1991) scaling relations would lead to any new insights about our simulation results nor that our simulations are relevant to their results. It would be interesting to investigate a spatial model as it scaled between the continuous population structure of Barton and Rouhani (1991) and the metapopulation structure of our model to determine how effects of stochastic migration vary along such a gradient of population structures. However, as we note below, our model was developed with insect agricultural pests in mind and it was felt that a metapopulation model was more appropriate than a continuous spatial model.

We have some additional qualms about Coyne et al.'s (2000) response to our paper. First, we never claimed ''there have been no theoretical analyses of the SBT in spatially extended populations'' (Coyne et al. 2000). Table 1 of Peck et al. (1998) clarifies that our complaint was the lack of discrete, stochastic stepping-stone models. We have serious reservations about *any* results from an island model being used to place limits on the requirements for SBT. Coyne et al. (2000) cite Rouhani and Barton (1993) to the effect that differential emigration from demes has a negligible effect on the spread of a new adaptive peak. However, that situation is for an island model where the differential emigration is diluted among all other demes, rather than being directed into a few neighbors where it can help push them through the adaptive valley.

Second, we urge caution in dismissing SBT because it is complex. Mass selection is admittedly a more simple and straightforward explanation of adaptive evolution that deserves to be taken as the null model. However, there is the danger that this simplicity is the reason for the preponderance of mass selection in the literature. Because mass selection is more easily tested in the field and in the laboratory, we would expect the literature to favor this mode of evolution (and as we have noted elsewhere [Ellner et al. 1999], the sample size is small: observations of selection response in natural, unmanipulated populations, other than responses to anthropogenic directional selection, are rare). For example, a side-by-side enumeration of cases where the simpler theory can adequately explain all observations would favor Newtonian physics over relativity. Similarly, Darwinian theories of speciation are complex and require a ''specific concatenation'' of ecological and genetic events (cf. Coyne et al. 2000, p. 308). Lacking direct observations of speciation, we therefore defend the theory ''by making separate arguments for each of its components, implicitly assuming that if each component can be seen, the theory as a whole must work in nature'' (Coyne et al. 2000, p. 306).

Although we agree with Coyne et al. (2000) that ultimately SBT must be evaluated based on its ability to account for observations, we cannot agree that a ''piecemeal'' defense of a complex theory is a priori unconvincing. We do not argue that SBT is the most frequent mode of evolution, but we believe that there are compelling reasons to believe that it should not be ignored; evidence that it may occur under less restrictive conditions than previous theory suggests is accruing (e.g., for a good combination of experiment and

theory that demonstrates the STB with stochastic migration, see Antonovics et al. 1997). More generally, the roles of stochastic variation and discrete, spatial population dynamics (Durrett and Levin 1994) need to be explored more thoroughly for much of evolutionary theory, not only in migration but in other aspects of life history as well. For example Dieckmann and Doebeli (1999) use an individual-based stochastic model to demonstrate how the waiting time to sympatric speciation based on assortative mating for a trait is affected by the number of loci determining the trait.

Finally, our interest in SBT does not derive from any kind of ''holism.'' It comes from our previous work on the rapid evolution of resistance to pesticides and to transgenic crops expressing the Bt endotoxin in insect agricultural pests. The potentially rapid spread of resistance to transgenic crops is both a puzzle and an urgent practical problem (Roush 1994; Gould 1998). Correctly identifying the mode of resistance evolution is essential if we are to defeat, or at least impede, the consistent efficiency of pest evolution at overcoming human defenses of our food supply. In a general strategic model (Peck and Ellner 1997) and a detailed spatial simulation model for *Heliothis virescens* in transgenic cotton (Peck et al. 1999), the spread of resistance involved spatial processes highly reminiscent of SBT. Once some fluke (of local conditions, initial allele frequencies, drift, etc.) allows the allele combination conferring resistance to become locally abundant somewhere, the tremendous selective advantage of resistance allows the resistant genotype to spread rapidly through the entire planted region. This process is consistent with Epperson (1995), who found, as in single-locus systems, two-locus spatially structured populations under isolation by distance (and stochastic migration) formed patches of double homozygotes that were maintained even under selectively neutral conditions. Under the strong selection imposed by pesticide treatments, such patches quickly grow to encompass the entire cultivated region. With new transgenic crops expressing multiple toxins, resistance is expected to require mutations at two or more loci, with intermedicate genotypes having lower fitness than either completely susceptible or completely resistant genotypes (Gould 1998). Our continued interest in SBT reflects our concern that the necessary conditions for SBT, limited though they may be, are nonetheless broad enough to cover significant agricultural acreage, where the evolutionary responses to pest management practices can have enormous economic impact.

Literature Cited

Antonovics, J., P. H. Thrall, and A. M. Jones. 1997. Genetics and the spatial ecology of species interactions: the *Silene-Ustilago* system. Pp. 158–180 *in* D. Tilman and P. Kareiva, eds., Spatial ecology: the role of space in population dynamics and interspecific interactions. Princeton Univ. Press. Princeton, NJ.

Barton, N. H., and S. Rouhani. 1991. The probability of fixation of a new karyotype in a continuous population. Evolution 45: 499–517.

Cappucino, N., and P. W. Price, eds. 1995. Population dynamics: new approaches and syntheses. Academic Press, New York.

Connell, J. H., and W. P. Sousa. 1983. On the evidence needed to judge ecological stability or persistence. Am. Nat. 121:789–824.

Coyne, J. A., N. H. Barton, and M. Turelli. 1997. Perspective: a critique of Sewall Wright's shifting balance theory of evolution. Evolution 51:643–671.

———. 2000. Is Wright's shifting balance process important in evolution? Evolution 54:306–317.

Dieckmann, U., and M. Doebeli. 1999. On the origin of species by sympatric speciation. Nature 400:354–357.

Durrett, R., and S. Levin. 1994. The importance of being discrete (and spatial). Theor. Popul. Biol. 46:363–394.

Ellner, S. P., N. G. Hairston, Jr., C. M. Kearns, and D. Babaï. 1999. The roles of fluctuating selection and long-term diapause in microevolution of diapause timing in a freshwater copepod. Evolution 53:111–122.

Epperson, B. K. 1995. Spatial structure of two-locus genotypes under isolation by distance. Genetics 140:365–375.

Gould, F. 1998. Sustainability of transgenic insecticidal cultivars: integrating pest genetics and ecology. Annu. Rev. Entomol. 43: 701–726.

Peck, S. L., and S. P. Ellner. 1997. The effect of economic thresholds and life-history parameters on the evolution of pesticide resistance in a regional setting. Am. Nat. 149:43–63.

Peck, S. L., S. P. Ellner, and F. Gould. 1998. A spatially explicit stochastic model demonstrates the feasibility of Wright's shifting balance theory. Evolution 52:1834–1839.

Peck, S. L., F. Gould, and S. P. Ellner. 1999. Spread of resistance in spatially extended regions of transgenic cotton: implications for management of *Heliothis virescens* (Lepidoptera: Noctuidae). J. Econom. Entomol. 92:1–16.

Root, R. B., and N. Cappucino. 1992. Patterns of population change and the organization of the insect community associated with goldenrod. Ecol. Monogr. 62:393–420.

Rouhani, S., and N. H. Barton. 1993. Group selection and the ''shifting balance.'' Genet. Res 61:127–136.

Roush, R. T. 1994. Managing pests and their resistance to *Bacillus thuringiensis*: can transgenic crops be better than sprays? Biocontrol Sci. Technol. 4:501–516.

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